AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph bridging page 13 and 14, beginning with "The Expect value is used as a convenient way ..." with the following amended paragraph:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, *e.g.*, ~~http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/~~ the website of National Center for Biotechnology Information ("NCBI"), education/blastinfo. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (*e.g.*, "NNNNNNNNNNNNNN") or the letter "X" in protein sequences (*e.g.*, "XXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996).

Please replace the paragraph at page 36, beginning at line 22 with "The presence of identifiable domains in NOV1 ..." with the following amended paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (~~http:www.ebi.ac.uk/interpro~~ the website of European Bioinformatics Institute, ebi.ac.uk/interpro). DOMAIN results for NOV1 as disclosed in Tables 1K-1L, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1K and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (|) and "strong" semi-conserved residues are indicated by grey shading

or by the sign (+). The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.